

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Goeddel, David V.
Rothe, Mike
- (ii) TITLE OF INVENTION: TRAF Inhibitors
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Merchant & Gould P.C.
 - (B) STREET: 80 South 8th Street, Suite 3200
 - (C) CITY: Minneapolis
 - (D) STATE: Minnesota
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 10/679,614
 - (B) FILING DATE: 10/03/2003
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Katherine M. Kowalchyk
 - (B) REGISTRATION NUMBER: 36,848
 - (C) REFERENCE/DOCKET NUMBER: 11669.172USD5
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/371-5311
 - (B) TELEFAX: 612/332-9800

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 413 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Asp	Lys	Asn	Ile	Gly	Glu	Gln	Leu	Asn	Arg	Ala	Tyr	Glu	Ala
1				5				10					15	
Phe	Arg	Gln	Ala	Cys	Met	Asp	Arg	Asp	Ser	Ala	Val	Arg	Glu	Leu
			20					25					30	
Gln	Gln	Lys	Thr	Glu	Asn	Tyr	Glu	Gln	Arg	Ile	Arg	Glu	Gln	Gln
			35					40					45	

Glu	Gln	Leu	Ser	Phe	Gln	Gln	Asn	Leu	Ile	Asp	Arg	Leu	Lys	Ser	50	55	60
Gln	Leu	Leu	Leu	Val	Asp	Ser	Ser	Arg	Asp	Asn	Ser	Tyr	Gly	Tyr	65	70	75
Val	Pro	Leu	Leu	Glu	Asp	Ser	Asp	Arg	Arg	Lys	Asn	Asn	Leu	Thr	80	85	90
Leu	Asp	Glu	Pro	His	Asp	Lys	Val	Lys	Leu	Gly	Thr	Leu	Arg	Asp	95	100	105
Lys	Gln	Ser	Lys	Val	Arg	Arg	Gln	Glu	Val	Ser	Ser	Gly	Lys	Glu	110	115	120
Ser	Ala	Lys	Gly	Leu	Asn	Ile	Pro	Leu	His	His	Glu	Arg	Asp	Asn	125	130	135
Ile	Glu	Lys	Thr	Phe	Trp	Asp	Leu	Lys	Glu	Glu	Phe	His	Arg	Ile	140	145	150
Cys	Leu	Leu	Ala	Lys	Ala	Gln	Lys	Asp	His	Leu	Ser	Lys	Leu	Asn	155	160	165
Ile	Pro	Asp	Ile	Ala	Thr	Asp	Thr	Gln	Cys	Ser	Val	Pro	Ile	Gln	170	175	180
Cys	Thr	Asp	Lys	Thr	Glu	Lys	Gln	Glu	Ala	Leu	Phe	Lys	Pro	Gln	185	190	195
Ala	Lys	Asp	Asp	Ile	Asn	Arg	Gly	Met	Ser	Cys	Val	Thr	Ala	Val	200	205	210
Thr	Pro	Arg	Gly	Leu	Gly	Arg	Asp	Glu	Glu	Asp	Thr	Ser	Phe	Glu	215	220	225
Ser	Leu	Ser	Lys	Phe	Asn	Val	Lys	Phe	Pro	Pro	Met	Asp	Asn	Asp	230	235	240
Ser	Ile	Phe	Leu	His	Ser	Thr	Pro	Glu	Ala	Pro	Ser	Ile	Leu	Ala	245	250	255
Pro	Ala	Thr	Pro	Glu	Thr	Val	Cys	Gln	Asp	Arg	Phe	Asn	Met	Glu	260	265	270
Val	Arg	Asp	Asn	Pro	Gly	Asn	Phe	Val	Lys	Thr	Glu	Glu	Thr	Leu	275	280	285
Phe	Glu	Ile	Gln	Gly	Ile	Asp	Pro	Ile	Thr	Ser	Ala	Ile	Gln	Asn	290	295	300
Leu	Lys	Thr	Thr	Asp	Lys	Thr	Asn	Pro	Ser	Asn	Leu	Arg	Ala	Thr	305	310	315
Cys	Leu	Pro	Ala	Gly	Asp	His	Asn	Val	Phe	Tyr	Val	Asn	Thr	Phe	320	325	330

Pro	Leu	Gln	Asp	Pro	Pro	Asp	Ala	Pro	Phe	Pro	Ser	Leu	Asp	Ser	335	340	345
Pro	Gly	Lys	Ala	Val	Arg	Gly	Pro	Gln	Gln	Pro	Phe	Trp	Lys	Pro	350	355	360
Phe	Leu	Asn	Gln	Asp	Thr	Asp	Leu	Val	Val	Pro	Ser	Asp	Ser	Asp	365	370	375
Ser	Glu	Leu	Leu	Lys	Pro	Leu	Val	Cys	Glu	Phe	Cys	Gln	Glu	Leu	380	385	390
Phe	Pro	Pro	Ser	Ile	Thr	Ser	Arg	Gly	Asp	Phe	Leu	Arg	His	Leu	395	400	405
Asn	Thr	His	Phe	Asn	Gly	Glu	Thr								410		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1955 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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CTGGAACGGA AAGCTACTTC CGGTTGCAGT CATTCTGCCG GGCACCGGCG 50
ACCTGTGGCG TGAGCGAGCA CAGCCGGAAC CCTCCACTAG CTGGCATTCC 100
TACCATCCTT TATAGTGATG CTACAGGACA AAGAGGAATG GATAAAAACA 150
TTGGTGAGCA ACTCAATAGA GCATATGAAG CCTTCCGACA GGCATGCATG 200
GATAGAGATT CAGCAGTAAG AGAGCTACAG CAAAAGCAGA CTGAGAACTA 250
TGAACAAAGA ATACGCGAGC AACAGGAACA GCTGTCATTT CAACAAAACC 300
TAATTGACAG GCTGAAATCA CAGCTACTTC TCGTGGATTC TAGTCGAGAT 350
AACAGTTATG GCTATGTACC TTTGCTTGAA GACAGTGACA GAAGGAAGAA 400
TAATTTGACC CTTGATGAAC CACATGATAA AGTGAAACTA GGAACACTGA 450
GAGATAAGCA ATCAAAGGTG AGACGACAAG AAGTTTCTTC TGGAAAAGAA 500
TCCGCCAAGG GTCTCAACAT CCCTCTGCAT CACGAAAGGG ATAATATAGA 550
GAAGACTTTC TGGGACCTTA AAGAAGAATT TCATAGGATT TGCTTGCTAG 600
CAAAAGCACA GAAAGATCAC TTAAGCAAAC TTAATATACC AGATATTGCA 650
ACTGACACAC AGTGTTCTGT GCCTATACAG TGTACTGATA AAACAGAGAA 700

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ACAAGAAGCG CTGTTTAAGC CCCAGGCTAA AGATGATATA AATAGAGGTA 750
 TGTCGTGCGT CACAGCTGTC ACACCAAGAG GACTGGGCCG GGATGAGGAA 800
 GATACCTCTT TTGAATCACT TTCTAAATTC AATGTCAAGT TTCCGCCTAT 850
 GGACAATGAC TCTATTTTTC TACATAGCAC TCCAGAGGCC CCGAGCATCC 900
 TTGCTCCTGC CACACCTGAG ACAGTGTGCC AGGACCGATT TAATATGGAA 950
 GTCAGAGACA ACCCAGGAAA CTTTGTAAAA ACAGAAGAAA CTTTATTTGA 1000
 AATTCAGGGA ATTGACCCCA TAACTTCAGC TATACAAAAC CTTAAAACAA 1050
 CTGACAAAAC AAACCCCTCA AATCTTAGAG CGACGTGTTT GCCAGCTGGA 1100
 GACCACAATG TGTTCTATGT AAATACGTTT CCACTTCAAG ACCCGCCTGA 1150
 CGCACCTTTT CCCTCACTGG ATTCCCAGG AAAGGCTGTC CGAGGACCAC 1200
 AGCAGCCCTT TTGGAAGCCT TTTCTTAACC AAGACACTGA CTTAGTGGTA 1250
 CCAAGTGATT CAGACTCAGA GCTCCTTAAA CCTCTAGTGT GTGAATTCTG 1300
 TCAAGAGCTT TTCCCACCAT CCATTACATC CAGAGGGGAT TTCTCCGGC 1350
 ATCTTAATAC ACACTTTAAT GGGGAGACTT AAATCACGTT TGAAAACAGA 1400
 CATATCATGT TCTCTGTGGT GGTTTTGGAT TTGTAACGCT AGAGAACGCT 1450
 TTCTCGTGAG CCAAATGTAA GATTGATTAT AAAGTTGTTA CTTTATCTTT 1500
 TAAGAGATCA TTTTGTATAG AACTATAACT CATTATATTA TTCATGTTTA 1550
 TACCTATAAT TTCTACATTT CAAAATTACA CATGTGACTT ACAGAGTTAT 1600
 TCAGTCATAA TTTATGTTTC AAATAGCTAA GTTTATTGTT TGACTATTGT 1650
 GAGATCTATT AAATTTAGTA ATAGCAAATG TTTATAGGAT ATTCAAATTT 1700
 CATTTGAATT TTTAATTATT TTTGCTACAG GTAATATTCC TTTAAAATAC 1750
 GTATATAACG TACAGAGAAT AACAGACAAT ATGATCTAAG TAAATGTCGA 1800
 ATCAATCATT AGTTGCCCAG GGAAATTTAA ACATTATAGA TCATTTTAA 1850
 ATAATACACA TAGTTTAAAT TTTTACTGTG TGTATAGATG CATGATTAAA 1900
 TGACTTAAAT ATTAAGAGTG ACTTACGTCG TGCTTATTAA AAAAAAAAAA 1950
 AAAAA 1955

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Ser Leu Lys Arg His Ser Leu Arg Arg Asn Ala Cys His Leu
 1             5             10             15
Glu Thr Arg Ala Gly Ile Pro Thr Ile Leu Tyr Ser Asp Ala Thr
             20             25             30
Gly Gln Arg Gly
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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CCCACGCGTC CGGTTTGGGC AGCATCTGTA GAGCCTGTGC AAACGGCTTC 50
CAGAATGGGT ACGTGCCTAT GTCTTTAAAG AGACATAGTC TGCGAAGGAA 100
CGCCTGTAC CTGGAGACGA GAGCTGGCAT TCCTACCATC CTTTATAGTG 150
ATGCTACAGG ACAAAGAGGA 170
```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 425 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Asp Lys Asn Ile Gly Glu Gln Leu Asn Lys Ala Tyr Glu Ala
 1             5             10             15
Phe Arg Gln Ala Cys Met Asp Arg Asp Ser Ala Val Lys Glu Leu
             20             25             30
Gln Gln Lys Thr Glu Asn Tyr Glu Gln Arg Ile Arg Glu Gln Gln
             35             40             45
Glu Gln Leu Ser Leu Gln Gln Thr Ile Ile Asp Lys Leu Lys Ser
             50             55             60
Gln Leu Leu Leu Val Asn Ser Thr Gln Asp Asn Asn Tyr Gly Cys
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65										70					75				
Val	Pro	Leu	Leu	Glu	Asp	Ser	Asp	Thr	Arg	Lys	Asn	Thr	Leu	Thr					
				80					85					90					
Leu	Ala	Gln	Pro	Gln	Asp	Lys	Val	Ile	Ser	Gly	Ile	Ala	Arg	Glu					
				95					100					105					
Lys	Leu	Pro	Lys	Val	Arg	Arg	Gln	Glu	Val	Ser	Ser	Pro	Arg	Lys					
				110					115					120					
Glu	Thr	Ser	Ala	Arg	Ser	Leu	Gly	Ser	Pro	Leu	Leu	His	Glu	Arg					
				125					130					135					
Gly	Asn	Ile	Glu	Lys	Thr	Ser	Trp	Asp	Leu	Lys	Glu	Glu	Phe	His					
				140					145					150					
Lys	Ile	Cys	Met	Leu	Ala	Lys	Ala	Gln	Lys	Asp	His	Leu	Ser	Lys					
				155					160					165					
Leu	Asn	Ile	Pro	Asp	Thr	Ala	Thr	Glu	Thr	Gln	Cys	Ser	Val	Pro					
				170					175					180					
Ile	Gln	Cys	Thr	Asp	Lys	Thr	Asp	Lys	Gln	Glu	Ala	Leu	Phe	Thr					
				185					190					195					
Pro	Gln	Ala	Lys	Asp	Asp	Ile	Asn	Arg	Gly	Ala	Pro	Ser	Ile	Thr					
				200					205					210					
Ser	Val	Thr	Pro	Arg	Gly	Leu	Cys	Arg	Asp	Glu	Glu	Asp	Thr	Ser					
				215					220					225					
Leu	Glu	Ser	Leu	Ser	Lys	Phe	Asn	Val	Lys	Phe	Pro	Pro	Met	Asp					
				230					235					240					
Asn	Asp	Ser	Thr	Phe	Leu	His	Ser	Thr	Pro	Glu	Arg	Pro	Gly	Ile					
				245					250					255					
Leu	Ser	Pro	Ala	Thr	Ser	Glu	Ala	Val	Cys	Gln	Glu	Lys	Phe	Asn					
				260					265					270					
Met	Glu	Phe	Arg	Asp	Asn	Pro	Gly	Asn	Phe	Val	Lys	Thr	Glu	Glu					
				275					280					285					
Thr	Leu	Phe	Glu	Ile	Gln	Gly	Ile	Asp	Pro	Ile	Ala	Ser	Ala	Ile					
				290					295					300					
Gln	Asn	Leu	Lys	Thr	Thr	Asp	Lys	Thr	Lys	Pro	Ser	Asn	Leu	Val					
				305					310					315					
Asn	Thr	Cys	Ile	Arg	Thr	Thr	Leu	Asp	Arg	Ala	Ala	Cys	Leu	Pro					
				320					325					330					
Pro	Gly	Asp	His	Asn	Ala	Leu	Tyr	Val	Asn	Ser	Phe	Pro	Leu	Leu					
				335					340					345					
Asp	Pro	Ser	Asp	Ala	Pro	Phe	Pro	Ser	Leu	Asp	Ser	Pro	Gly	Lys					

	350		355		360
Ala Ile Arg Gly	Pro Gln Gln Pro Ile	Trp Lys Pro Phe Pro	Asn		
	365	370	375		
Gln Asp Ser Asp	Ser Val Val Leu Ser	Gly Thr Asp Ser Glu	Leu		
	380	385	390		
His Ile Pro Arg	Val Cys Glu Phe Cys	Gln Ala Val Phe Pro	Pro		
	395	400	405		
Ser Ile Thr Ser	Arg Gly Asp Phe Leu	Arg His Leu Asn Ser	His		
	410	415	420		
Phe Asn Gly Glu Thr					
	425				

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2108 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

GTTTGAGCAG CATTTGTTAGA GCCTGTGGAA AACACTTTTAC AACTGTGTAA 50
CTGTCTTCAT CTTTACAGAG GAATAGTCTA CAAAGGAAGA CTTGTAACCT 100
GGAGAAGAGA CCTGTCATTT ACTCCATCCT TTATAGTGAT GCTACAGGAC 150
GAAGAGGAAT GGATAAAAAC ATTGGCGAGC AACTCAATAA AGCGTATGAA 200
GCCTTCCGGC AGGCATGCAT GGATAGAGAT TCTGCAGTAA AAGAATTACA 250
GCAAAAGACT GAGAACTATG AGCAGAGAAT ACGTGAACAA CAGGAACAGC 300
TGTCACTCCA ACAGACTATT ATTGACAAGC TAAAATCTCA GTTACTTCTT 350
GTGAATTCCA CTCAAGATAA CAATTATGGC TGTGTCCCTC TGCTTGAAGA 400
CAGTGACACA AGAAAGAATA CTTTGACTCT TGCTCAGCCA CAAGATAAAG 450
TGATTTTCAGG AATAGCAAGA GAAAAACTAC CAAAGGTAAG AAGACAAGAG 500
GTTTCTTCTC CTAGAAAAGA AACTTCAGCA AGGAGTCTTG GCAGTCCTTT 550
GCTCCATGAA AGGGGTAATA TAGAGAAGAC TTCCTGGGAT CTGAAAGAAG 600
AATTTCATAA AATATGCATG CTAGCAAAAG CACAGAAAGA CCACTTAAGC 650
AAACTTAATA TACCAGACAC TGCAACTGAA ACACAGTGCT CTGTGCCTAT 700
ACAGTGACG GATAAAACAG ATAAACAAGA AGCGCTGTTT ACGCCTCAGG 750

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CTAAAGATGA TATAAATAGA GGTGCACCAT CCATCACATC TGTCACACCA 800
AGAGGACTGT GCAGAGATGA GGAAGACACC TCTTTGGAAT CACTTTCTAA 850
ATTCAATGTC AAGTTTCCAC CTATGGACAA TGA CTCAACT TTCTTACATA 900
GCACTCCAGA GAGACCCGGC ATCCTTAGTC CTGCCACGTC TGAGGCAGTG 950
TGCCAAGAGA AATTTAATAT GGAGTTCAGA GACAACCCAG GGAAC TTTGT 1000
TAAACAGAA GAACTTTTAT TTGAAATTCA GGAATTGAC CCCATAGCTT 1050
CAGCTATACA AACCTTAAA ACAACTGACA AAACAAAGCC CTC AAATCTC 1100
GTAAACACTT GTATCAGGAC AACTCTGGAT AGAGCTGCGT GTTTGCCACC 1150
TGGAGACCAT AATGCATTAT ATGTAAATAG CTTCCCACTT CTGGACCCAT 1200
CTGATGCACC TTTTCCCTCA CTCGATTCCC CGGGAAAAGC AATCCGAGGA 1250
CCACAGCAGC CCATTTGGAA GCCCTTTCCT AATCAAGACA GTGACTCGGT 1300
GGTACTAAGT GGCACAGACT CAGAACTGCA TATACCTCGA GTATGTGAAT 1350
TCTGTCAAGC AGTTTTCCCA CCATCCATTA CATCCAGGGG GGATTTCCCTT 1400
CGGCATCTTA ATTCACACTT CAATGGAGAG ACTTAAGACA CATTTGAAAA 1450
CAGACATATC AAGTTCTATG TGATGATTTT GGGTTTTTAA TACTATAAAT 1500
ACTTGATTGT AAATAAATT CAAGATCATT TATAGGAAAA TCTAGTTTCA 1550
CAGCTATTTG AATTTTTTTC TGGATTACT ATATAACTCT TATTTTTTAA 1600
AAGATCATTC TGTTCTTTCA AGGAGAAATA AGCCTAAAAG AAGAAAAACA 1650
AAAAAATTC TGTATAAAAC TGTAATCCTT TGTATTCATG TTTACAGTGC 1700
TATTACTATA ATTCAAAATT ATGTATGTGA CTTAGAGTTA TATAATCATA 1750
ATTTATGTTT ATTTCAAATA TCTAAGTTTA TTGCTTGGAT TTCTAGTGAG 1800
AGCTGTTGAA TTTGGTGATG TCAAATGTTT CTAGGGTTTT TTAGTTTGTT 1850
TTTATTGAGA AAATTGATTA TTTATGCTAT AGGTGATATT CTCTTTGAAT 1900
AAACCTATAA TAGGAAATAG CAGACCACAT AAACATCTTT GTAAATATCA 1950
AACCTAATAC ATTTCTTGTC CAGTGATAAA ACAACTGGTA GAATTATTTA 2000
AACACTTTAG ATTTTAAAT AATAAACATG GCTTTAATTT TTAGTGTTG 2050
TATAGCTACA TGATGAAATT AATTAAATAT TAAGAGGTAA AAAAAAAAAA 2100
AAAAAAAA 2108

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1922 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
CGGAAAGCTA CTTCCGGTTG CAGTCATTCT GCCGGGCACC GGCGACCTGT 50
GGCGTGAGCG AGCACAGCCG GAACCCTCCA CTAGCTGGCA TTCCTACCAT 100
CCTTTATAGT GATGCTACAG GACAAAGAGG AATGGATAAA AACATTGGTG 150
AGCAACTCAA TAGAGCATAT GAAGCCTTCC GACAGGCATG CATGGATAGA 200
GATTCAGCAG TAAGAGAGCT ACAGCAAAAG CAGACTGAGA ACTATGAACA 250
AAGAATACGC GAGCAACAGG AACAGCTGTC ATTTCAACAA AACCTAATTG 300
ACAGGCTGAA ATCACAGCTA CTTCTCGTGG ATTCTAGTCG AGATAACAGT 350
TATGGCTATG TACCTTTGCT TGAAGACAGT GACAGAAGGA AGAATAATTT 400
GACCCTTGAT GAACCACATG ATAAAGTGAA ACTAGGAACA CTGAGAGATA 450
AGCAATCAAA GGTGAGACGA CAAGAAGTTT CTTCTGGAAA AGAATCCGCC 500
AAGGGTCTCA ACATCCCTCT GCATCACGAA AGGGATAATA TAGAGAAGAC 550
TTTCTGGGAC CTTAAAGAAG AATTTCATAG GATTTGCTTG CTAGCAAAAG 600
CACAGAAAGA TCACTTAAGC AAACCTAATA TACCAGATAT TGCAACTGAC 650
ACACAGTGTT CTGTGCCTAT ACAGTGTA CTGATAAAACAG AGAAACAAGA 700
AGCGCTGTTT AAGCCCCAGG CTAAAGATGA TATAAATAGA GGTATGTCGT 750
GCGTCACAGC TGTCACACCA AGAGGACTGG GCCGGGATGA GGAAGATACC 800
TCTTTTGAAT CACTTTCTAA ATTCAATGTC AAGTTTCCGC CTATGGACAA 850
TGACTCTATT TTTCTACATA GCACTCCAGA GGCCCCGAGC ATCCTTGCTC 900
CTGCCACACC TGAGACAGTG TGCCAGGACC GATTTAATAT GGAAGTCAGA 950
GACAACCCAG GAACTTTTGT TAAAACAGAA GAACTTTTAT TTGAAATTCA 1000
GGGAATTGAC CCCATAACTT CAGCTATACA AAACCTTAAA ACAACTGACA 1050
AAACAAACCC CTCAAATCTT AGAGCGACGT GTTTGCCAGC TGGAGACCAC 1100
AATGTGTTCT ATGTAAATAC GTTCCCACTT CAAGACCCGC CTGACGCACC 1150
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TTTTCCCTCA CTGGATTCCC CAGGAAAGGC TGTCCGAGGA CCACAGCAGC 1200
 CCTTTTGGAA GCCTTTTCTT AACCAAGACA CTGACTTAGT GGTACCAAGT 1250
 GATTCAGACT CAGAGCTCCT TAAACCTCTA GTGTGTGAAT TCTGTCAAGA 1300
 GCTTTTCCCA CCATCCATTA CATCCAGAGG GGATTTCCTC CGGCATCTTA 1350
 ATACACACTT TAATGGGGAG ACTTAAATCA CGTTTGAAAA CAGACATATC 1400
 ATGTTCTCTG TGGTGGTTTT GGATTTGTAA CGCTAGAGAA CGCTTTCTCG 1450
 TGAGCCAAAT GTAAGATTGA TTATAAAGTT GTTACTTTAT CTTTTAAGAG 1500
 ATCATTTTGT ATAGAACTAT AACTCATTAT ATTATTCATG TTTATACCTA 1550
 TAATTTCTAC ATTTCAAAAT TACACATGTG ACTTACAGAG TTATTCAGTC 1600
 ATAATTTATG TTTCAAATAG CTAAGTTTAT TGTTTGACTA TTGTGAGATC 1650
 TATTAAATTT AGTAATAGCA AATGTTTATA GGATATTCAA ATTTCATTTG 1700
 AATTTTAAAT TATTTTGTCT ACAGGTAATA TTCCTTTAAA ATACGTATAT 1750
 AACGTACAGA GAATAACAGA CAATATGATC TAAGTAAATG TCGAATCAAT 1800
 CATTAGTTGC CCAGGGAAAT TTAAACATTA TAGATCATTT TTAAATAATA 1850
 CACATAGTTT TAATTTTAC TGTGTGTATA GATGCATGAT TAAATGACTT 1900
 AAATATTAAA AAAAAAAAAA AA 1922

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2160 base pairs
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGCGACCTG TGGCGTGAGC GAGCACAGCC GGAACCCCTCC ACTAGCTGGC 50
 ATTCCTACCA TCCTTTATAG TGATGCTACA GGACAAAGAG GAATGGATAA 100
 AAACATTGGT GAGCAACTCA ATAGAGCATA TGAAGCCTTC CGACAGGCAT 150
 GCATGGATAG AGATTCAGCA GTAAGAGAGC TACAGCAAAA GACTGAGAAC 200
 TATGAACAAA GAATACGCGA GCAACAGGAA CAGCTGTCAT TTCAACAAAA 250
 CCTAATTGAC AGGCTGAAAT CACAGCTACT TCTCGTGGAT TCTAGTCGAG 300
 ATAACAGTTA TGGCTATGTA CCTTTGCTTG AAGACAGTGA CAGAAGGAAG 350

AATAATTTGA CCCTTGATGA ACCACATGAT AAAGTGAAAC TAGGAACACT 400
GAGAGATAAG CAATCAAAGG TGAGACGACA AGAAGTTTCT TCTGGAAAAG 450
AATCCGCCAA GGGTCTCAAC ATCCCTCTGC ATCACGAAAG GGATAATATA 500
GAGAAGACTT TCTGGGACCT TAAAGAAGAA TTTCATAGGA TTTGCTTGCT 550
AGCAAAAGCA CAGAAAGATC ACTTAAGCAA ACTTAATATA CCAGATATTG 600
CAACTGACAC ACAGTGTTCT GTGCCTATAC AGTGTACTGA TAAAACAGAG 650
AAACAAGAAG CGCTGTTTAA GCCCCAGGCT AAAGATGATA TAAATAGAGG 700
TATGTCGTGC GTCACAGCTG TCACACCAAG AGGACTGGGC CGGGATGAGG 750
AAGATACCTC TTTTGAATCA CTTTCTAAAT TCAATGTCAA GTTTCGCCT 800
ATGGACAATG ACTCTATTTT TCTACATAGC ACTCCAGAGG CCCCAGCAT 850
CCTTGCTCCT GCCACACCTG AGACAGTGTG CCAGGACCGA TTTAATATGG 900
AAGTCAGAGA CAACCCAGGA AACTTTGTTA AAACAGAAGA AACTTTATTT 950
GAAATTCAGG GAATTGACCC CATAACTTCA GCTATACAAA ACCTTAAAAC 1000
AACTGACAAA ACAAACCCCT CAAATCTTAG AGCGACGTGT TTGCCAGCTG 1050
GAGACCACAA TGTGTTCTAT GTAAATACGT TCCCATTCA AGACCCGCCT 1100
GACGCACCTT TTCCCTCACT GGATTCCCCA GGAAAGGCTG TCCGAGGACC 1150
ACAGCAGGTA ACTGTTTTGC ATTAACAAAT ATTTTATTAT GTGTGAACAC 1200
ACATTTTATC ATACATGTAC AGATACAAAT CTGTTTTAAG TTATCAGGCA 1250
TCCATTTAAA ATTAATGACT ATCCAGAGTT GAGGCTTTCA ATAAAAATATG 1300
TAAGTTCTGT ATTCAAGGAC ATGAATTTTG AATGTGACTG CGCTAAAGCT 1350
TCCTTGTGAT ACTGTGGCGT GGCTTTCCCT GCTTCGTCCT CTTCAAGCAC 1400
AGCTTGTTGA CATCAGTGCT CTAATGGATG CTTTATTAAA GTCAGTTACA 1450
GGCAGTAAAT AATTTTTTTA AAACCTGTGT AGGTACACAT AATAATGTGT 1500
AATTTTCCAT AAGTAGATAA TTGCACCAAA TATTCAAAAT AAACGTGCAT 1550
TCAGCCTACT TGTGTTACAT TTCTAGTTAC AGCAGTACAG AGGTCTGTAG 1600
TGTTTGTTTT GTTTACTAAC CTGACACTAA GCAGATATCC TTATACAGTT 1650
TTCAAATAAT CCCTGCACAT GAATACTGTA ATCAAATCTC TTCTTTACTG 1700
TTTGTGAAGC ACAAAGACTT TATAGCCCAT GAATCTAATC CTACCATCCT 1750
TTCTTCCAGA TTCAGGTTCT TTCACAGAAA TATTCCTTTT TGTTAGGAAG 1800

AAAAAAAGTT TTGTTTAATT TCTGAAGGTA AATGCTAAGT GTAGAAATGT 1850
 TAAAATAAAT AGAAGCATCT CATTAGAACT TTCAAACATT TGATTTTCTA 1900
 TCAGATTAAA AAAAATACTT AATACCTTTG GTTTACGTAT TCCTATCAGT 1950
 TATAGGCTTT TTGAACAGCA TGGAAAGAAG CAATAGTGAA GCTGTAGGAT 2000
 GTCTTAGTAG TGGGCGTAAG TAGAGATTCT GACAAGTCTT AATTATTAAC 2050
 TCTCTTATGT TCCACCCTGT ACCTTATTTT ACTTTATGGT CTCAGCTATA 2100
 GTTGCTACCA AATGAAACAA TTAAACAATT TCATGTGTTG CGAAAAAAAA 2150
 AAAAAAAAAA 2160

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Asp	Lys	Asn	Ile	Gly	Glu	Gln	Leu	Asn	Arg	Ala	Tyr	Glu	Ala	1	5	10	15
Phe	Arg	Gln	Ala	Cys	Met	Asp	Arg	Asp	Ser	Ala	Val	Arg	Glu	Leu	20	25	30	
Gln	Gln	Lys	Thr	Glu	Asn	Tyr	Glu	Gln	Arg	Ile	Arg	Glu	Gln	Gln	35	40	45	
Glu	Gln	Leu	Ser	Phe	Gln	Gln	Asn	Leu	Ile	Asp	Arg	Leu	Lys	Ser	50	55	60	
Gln	Leu	Leu	Leu	Val	Asp	Ser	Ser	Arg	Asp	Asn	Ser	Tyr	Gly	Tyr	65	70	75	
Val	Pro	Leu	Leu	Glu	Asp	Ser	Asp	Arg	Arg	Lys	Asn	Asn	Leu	Thr	80	85	90	
Leu	Asp	Glu	Pro	His	Asp	Lys	Val	Lys	Leu	Gly	Thr	Leu	Arg	Asp	95	100	105	
Lys	Gln	Ser	Lys	Val	Arg	Arg	Gln	Glu	Val	Ser	Ser	Gly	Lys	Glu	110	115	120	
Ser	Ala	Lys	Gly	Leu	Asn	Ile	Pro	Leu	His	His	Glu	Arg	Asp	Asn	125	130	135	
Ile	Glu	Lys	Thr	Phe	Trp	Asp	Leu	Lys	Glu	Glu	Phe	His	Arg	Ile	140	145	150	

Cys	Leu	Leu	Ala	Lys	Ala	Gln	Lys	Asp	His	Leu	Ser	Lys	Leu	Asn	155	160	165
Ile	Pro	Asp	Ile	Ala	Thr	Asp	Thr	Gln	Cys	Ser	Val	Pro	Ile	Gln	170	175	180
Cys	Thr	Asp	Lys	Thr	Glu	Lys	Gln	Glu	Ala	Leu	Phe	Lys	Pro	Gln	185	190	195
Ala	Lys	Asp	Asp	Ile	Asn	Arg	Gly	Met	Ser	Cys	Val	Thr	Ala	Val	200	205	210
Thr	Pro	Arg	Gly	Leu	Gly	Arg	Asp	Glu	Glu	Asp	Thr	Ser	Phe	Glu	215	220	225
Ser	Leu	Ser	Lys	Phe	Asn	Val	Lys	Phe	Pro	Pro	Met	Asp	Asn	Asp	230	235	240
Ser	Ile	Phe	Leu	His	Ser	Thr	Pro	Glu	Ala	Pro	Ser	Ile	Leu	Ala	245	250	255
Pro	Ala	Thr	Pro	Glu	Thr	Val	Cys	Gln	Asp	Arg	Phe	Asn	Met	Glu	260	265	270
Val	Arg	Asp	Asn	Pro	Gly	Asn	Phe	Val	Lys	Thr	Glu	Glu	Thr	Leu	275	280	285
Phe	Glu	Ile	Gln	Gly	Ile	Asp	Pro	Ile	Thr	Ser	Ala	Ile	Gln	Asn	290	295	300
Leu	Lys	Thr	Thr	Asp	Lys	Thr	Asn	Pro	Ser	Asn	Leu	Arg	Ala	Thr	305	310	315
Cys	Leu	Pro	Ala	Gly	Asp	His	Asn	Val	Phe	Tyr	Val	Asn	Thr	Phe	320	325	330
Pro	Leu	Gln	Asp	Pro	Pro	Asp	Ala	Pro	Phe	Pro	Ser	Leu	Asp	Ser	335	340	345
Pro	Gly	Lys	Ala	Val	Arg	Gly	Pro	Gln	Val	Thr	Val	Leu	His		350	355	359